

FIG. 1

0991258-11501

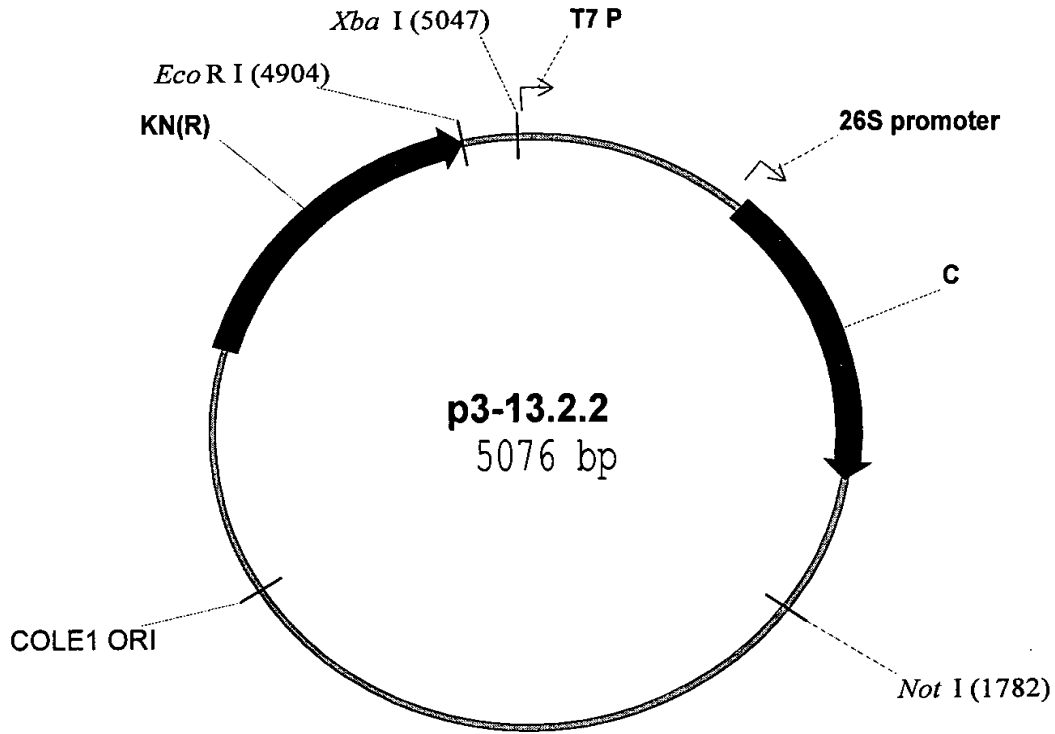


FIG. 2

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 "FOOT" 85215660

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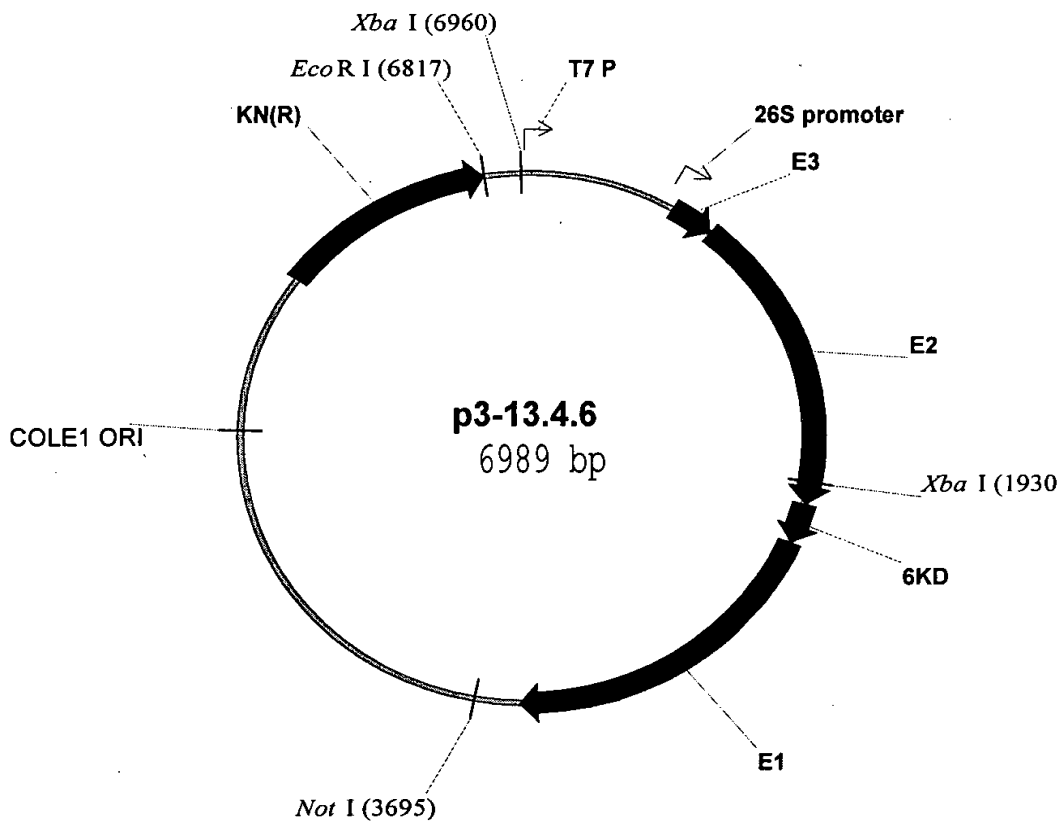


FIG. 3

0991258 11601
"FO9T" 85216660

APPROVED	C. FIG.	
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DRAFTSMAN		

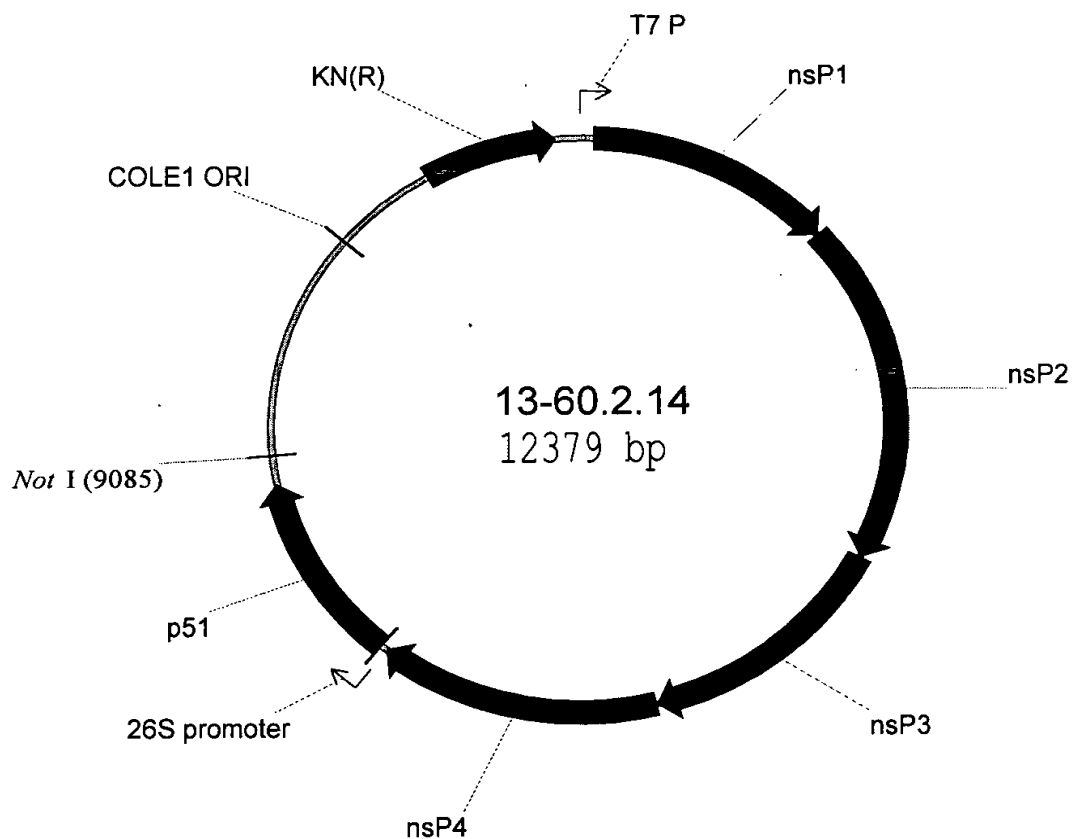


FIG. 4

0991258-11601
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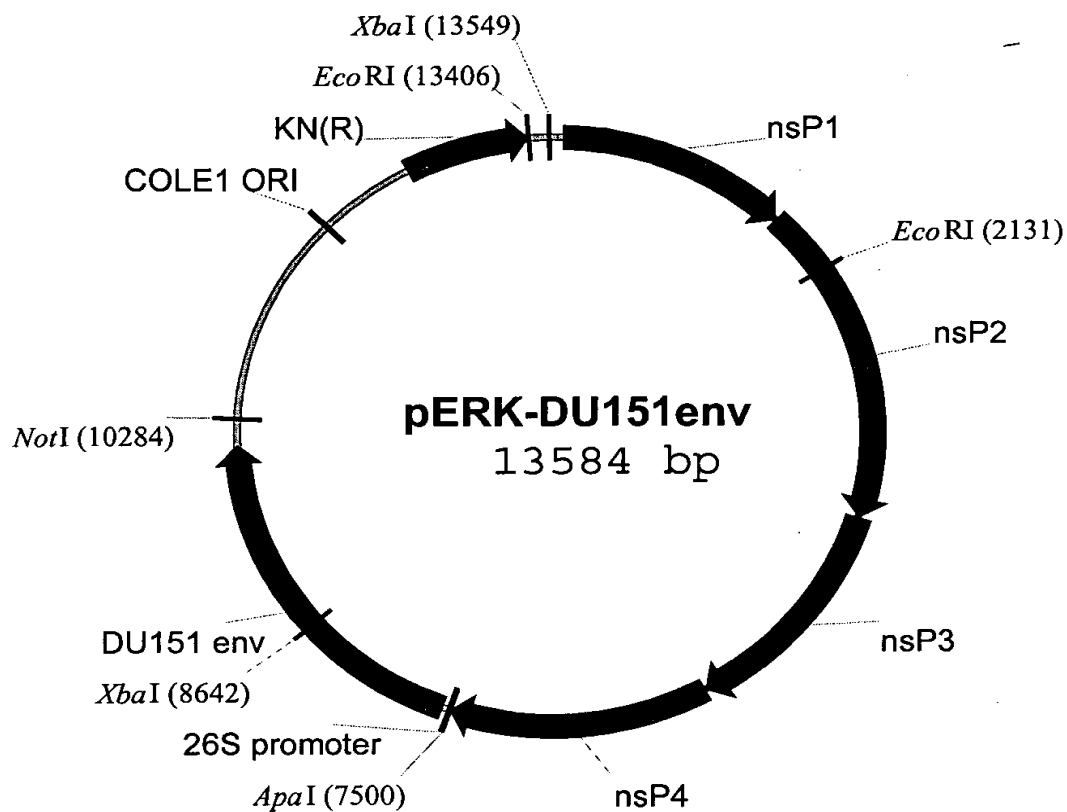


FIG. 5

1091113.0001U3 1.1.601

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1 2 3

kDa

202

132

72

42

32

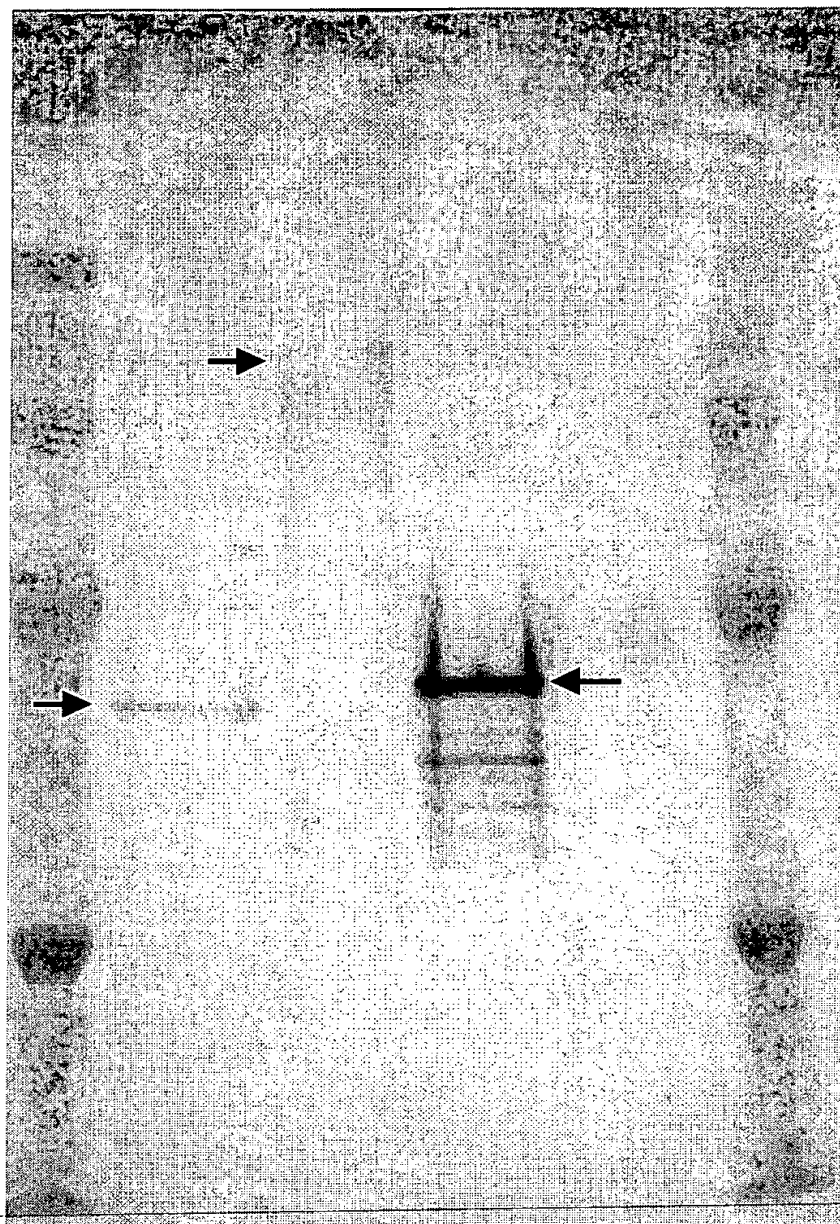


FIG. 6

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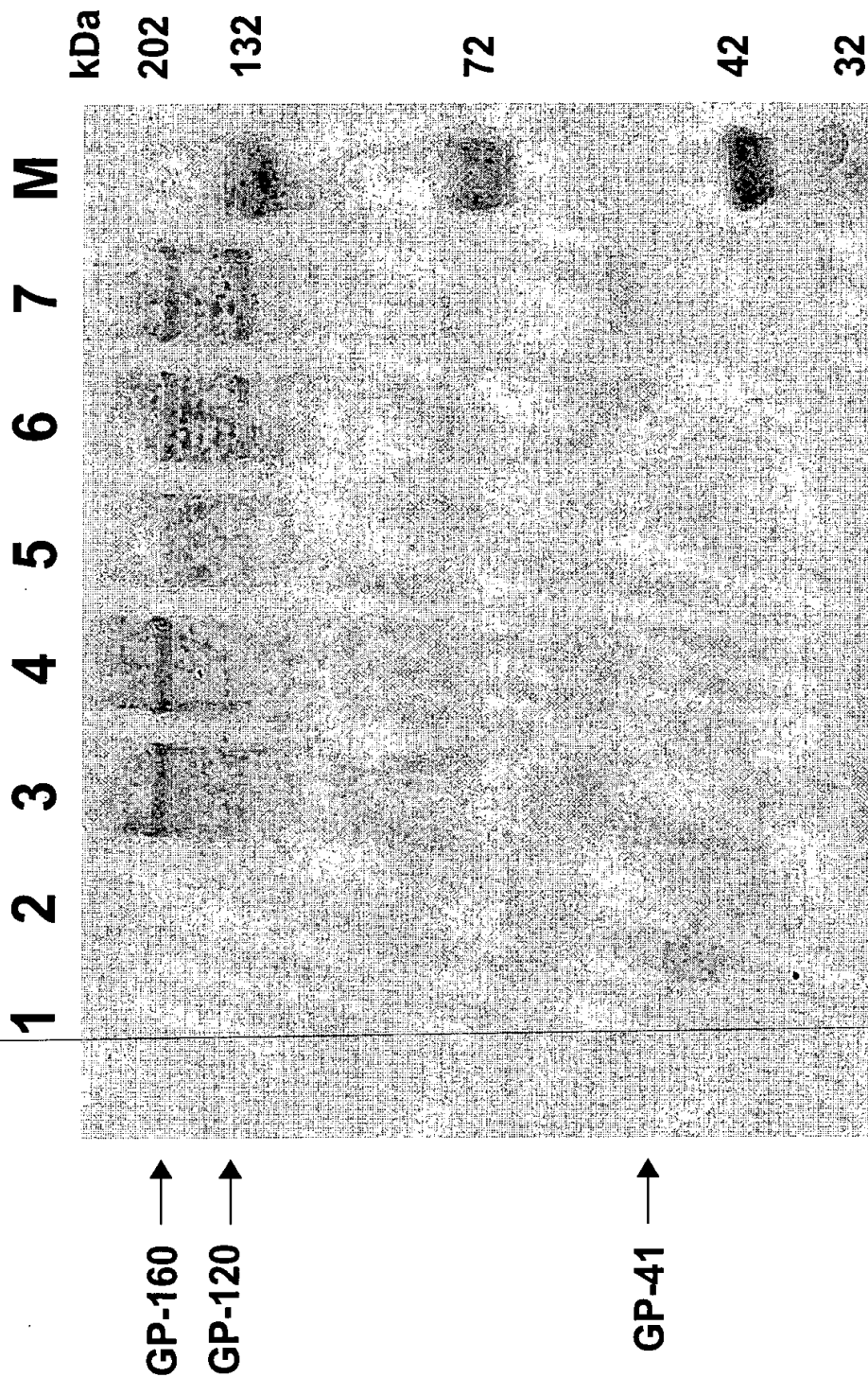


FIG. 7

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 Sheet 8 of 15

FO9TTF"852T6660

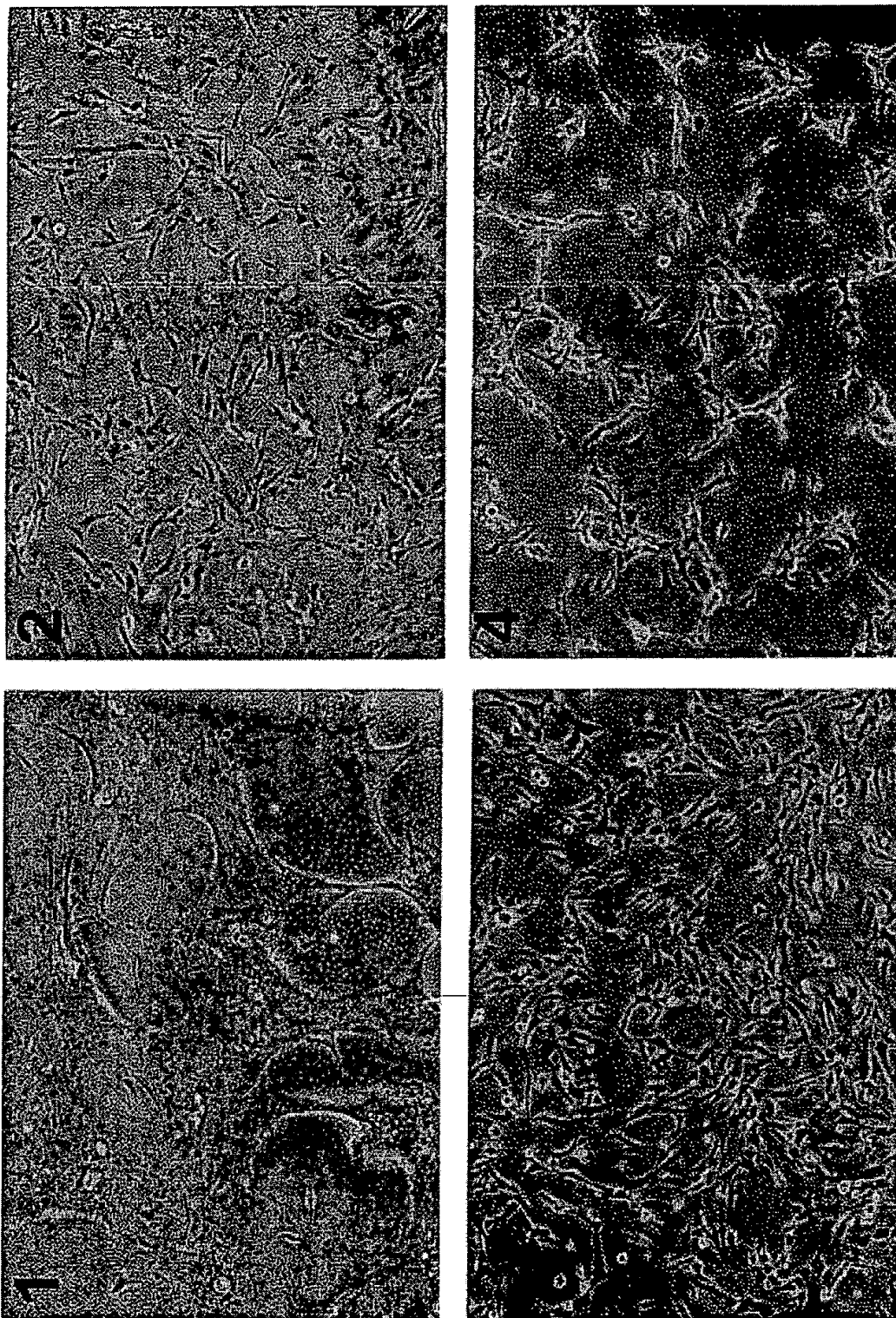


FIG. 8

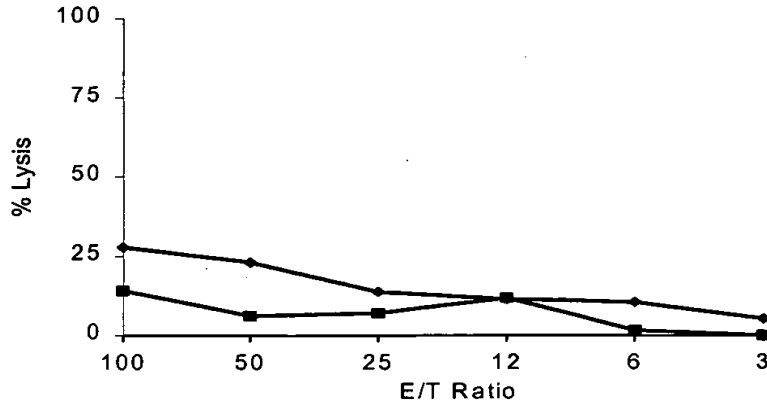


FIG. 9A

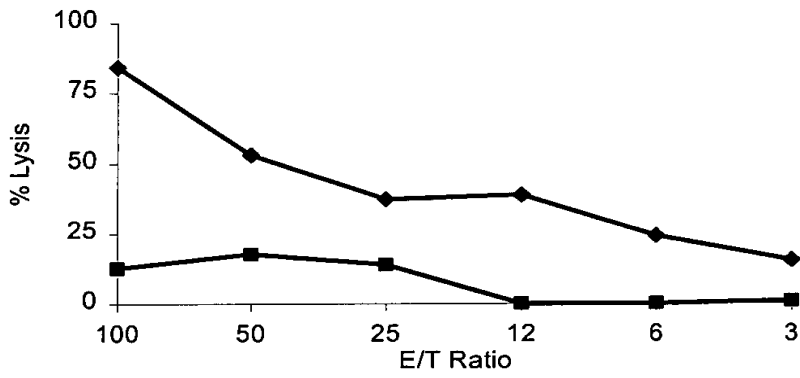


FIG. 9B

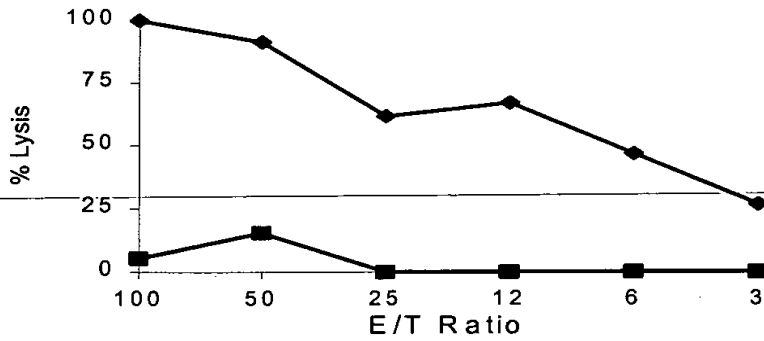


FIG. 9C

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Phylogenetic tree of HIV-1 gag sequences. The tree is rooted at the top and branches downwards. The central node is labeled 'Gag'. The tree is divided into two main clusters. The left cluster contains sequences such as DU174 gag, DU204 gag, CTSC1 gag, DU172 gag, RB21 gag, DU258 gag, DU179 gag, GG10 gag, DU123 gag, RB12 gag, DU156 gag, GG5 gag, RB13 gag, DU467 gag, GG3 gag, RB14 gag, and RB18 gag. The right cluster contains sequences such as CTSC2 gag, GG6 gag, DU368 gag, DU115 gag, RB22 gag, RB457 gag, DU281 gag, DU15 gag, RB15 gag, RB28 gag, RB1 gag, GG1 gag, GG4 gag, RB27 gag, RB28 gag, RB1 gag, GG1 gag, GG4 gag, RB27 gag, RB28 gag, RB1 gag, GG1 gag, GG4 gag, RB27 gag, RB28 gag, RB1 gag, GG1 gag, GG4 gag. The legend indicates that asterisks (*) denote consensus sequences, and arrows (→) denote vaccine candidates. Sequences marked with both are gag clones. The sequences marked with an asterisk are: Cgagcon, Malgagcon, DU422 gag, ES2 gag, SAgagcon, Dgagcon, Bgagcon, and Agagcon. The sequences marked with an arrow are: DU422 gag, ES2 gag, SAgagcon, and RB27 gag. The sequences marked with both are: DU422 gag, ES2 gag, SAgagcon, and RB27 gag.

FIG. 11

FIG. 12

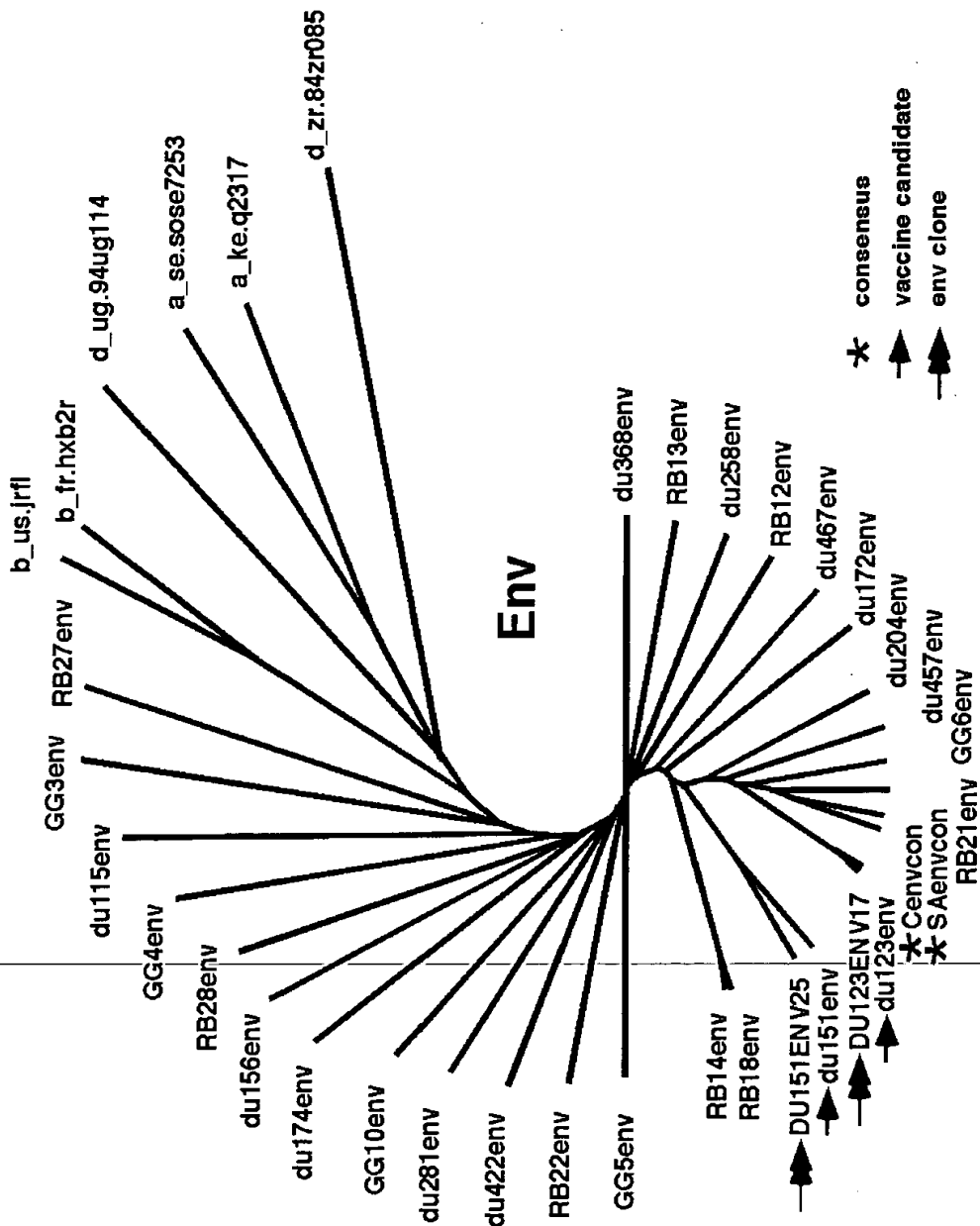


FIG. 12

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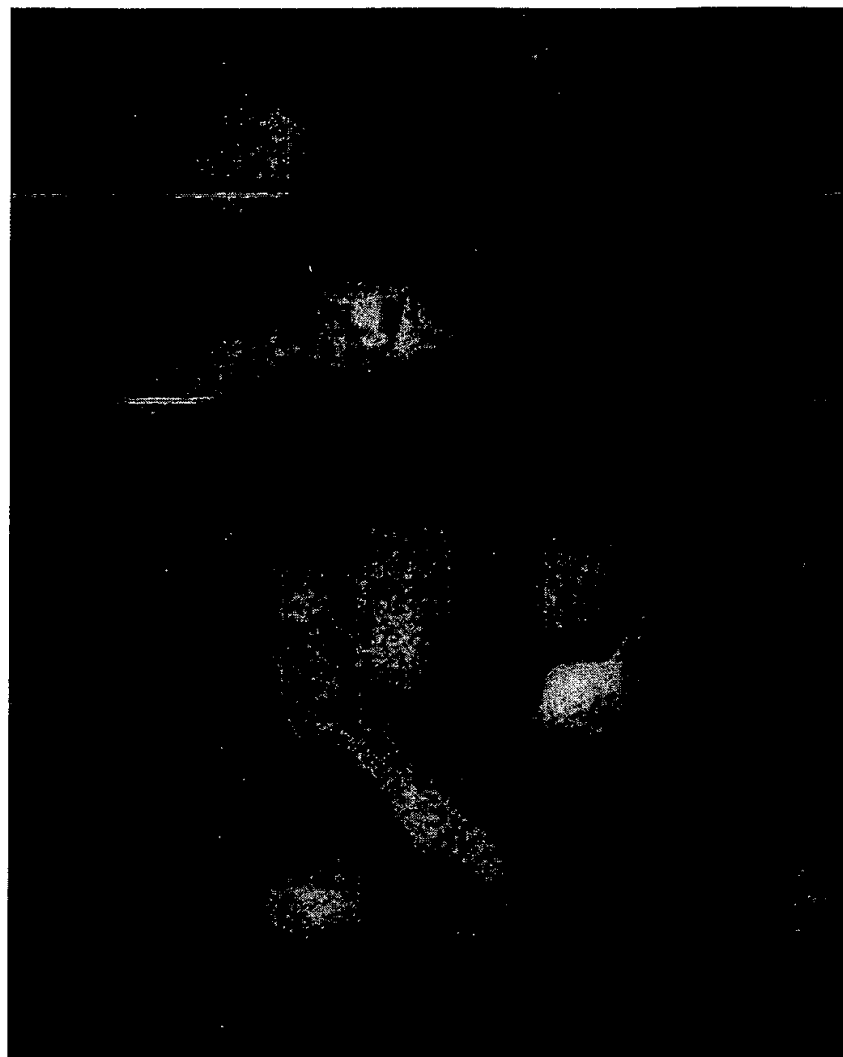


FIG. 14

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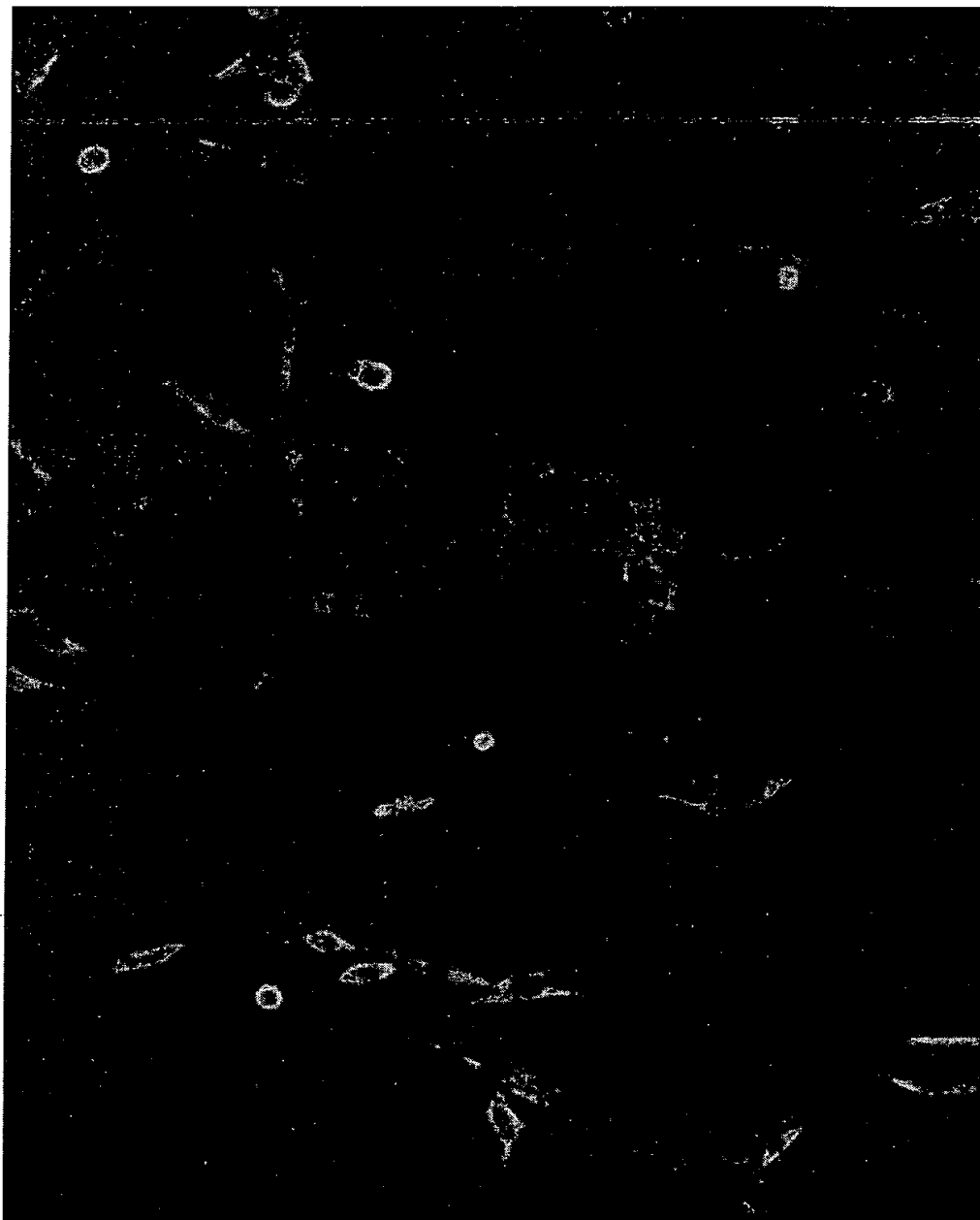


FIG. 15